

1/47

**FIG. 1A-1.**

**FIG. 1A-1.**

2/47

hB7-1	RIYQKQKMKVLTMMSCMN-----IWPEYKNTIF---DII--NNLSIVILALRPSDEETIEGVVLKYE	122
hB7-2	VVFQDDQENLVNEVYLGKEK--FDSVHSKVMRISF---D-S-DSWTIRLNLOIKKLVQIIHHKK	110
hB7P-1	YVYVQTSESKTIVV-TYHIPQNSSLENVDSRYRNALMSPAQMRLRDESLRFNVTIPQDEQKFHQLV-LSQ	118
hB7P-2	NIIQLTDTKQIVHSFQEQDQG-----SAMANRIALFPDQLAQENASRLQRVRVADEESFTGFV-SIR	127
hB7-H1	AIIVYWEMEDKNIIQFVHDEEDL-KVQHSSYRQPARLKQQLSLQENAAQITDVKLQDAQVPRGMI-SYCE	119
hB7-H2 long	AITA-----SLOKV-ENDTSHRERATLLEEQPLCKASFHPQVQVRDEEQVQII-IYCE	107
hB7-H2 short	AITA-----SLOKV-ENDTSHRERATLLEEQPLCKASFHPQVQVRDEEQVQII-IYCE	107
hB1N prot	EVRFKRVKVSVALVHRDQRQDA-AEQMPEYRGRATLVQDQAKLRVALRIRGARVSDDEMTICF--RED	129
hB1N2A1 prot	EVRFKRVKVSVALVHRDQRQDA-AEQMPEYRGRATLVQDQAKLRVALRIRGARVSDDEMTICF--RED	130
hB1N2A2 prot	EVRFKRVKVSVALVHRDQRQDA-AEQMPEYRGRATLVQDQAKLRVALRIRGARVSDDEMTICF--RED	134
hB1N3A2 prot	EVRFKRVKVSVALVHRDQRQDA-AEQMPEYRGRATLVQDQAKLRVALRIRGARVSDDEMTICF--RED	131
hB12.1 prot	EVRFKRVKVSVALVHRDQRQDA-AEQMPEYRGRATLVQDQAKLRVALRIRGARVSDDEMTICF--RED	130
hB13.2 prot	EVRFKRVKVSVALVHRDQRQDA-AEQMPEYRGRATLVQDQAKLRVALRIRGARVSDDEMTICF--RED	131
hB13.3 prot	EVRFKRVKVSVALVHRDQRQDA-AEQMPEYRGRATLVQDQAKLRVALRIRGARVSDDEMTICF--RED	131
hB1N3A3 prot (hB73)	EVRFKRVKVSVALVHRDQRQDA-AEQMPEYRGRATLVQDQAKLRVALRIRGARVSDDEMTICF--RED	131
hB1N3A1 prot	EVRFKRVKVSVALVHRDQRQDA-AEQMPEYRGRATLVQDQAKLRVALRIRGARVSDDEMTICF--RED	131
hB1F5 prot	EVRFKRVKVSVALVHRDQRQDA-AEQMPEYRGRATLVQDQAKLRVALRIRGARVSDDEMTICF--RED	131
hB7.3	EVRFKRVKVSVALVHRDQRQDA-AEQMPEYRGRATLVQDQAKLRVALRIRGARVSDDEMTICF--RED	129

FIG. 1A-2.

**FIG. 1A-3.**

Alignment Report of hB7 lineage, using Clustal method with PAM250 residue weight table.

hB7-1	INTT	VSQ	PETEL	YAVSSKLD	---	NMTTNH	SFMC	L	I	K	Y	G	221																																																		
hB7-2	IMQK	-SQ	ENVTE	YDVSIS	SVS	---	P	D	V	T	S	N	M	T	I	F	C	I	E	L	T	D	217																																								
hB7-1	LQND	T	F	LNMR	G	Y	D	W	S	V	L	R	I	A	R	T	P	S	V	N	I	G	C	C	I	E	N	V	L	Q	Q	N	L	V	G	S	Q	T	G	N	D	235																					
hB7-2	TTSQ	M	A	---	NEQ	G	F	D	H	S	V	L	R	V	L	G	A	N	G	T	Y	S	C	L	V	R	N	P	V	Q	Q	D	-	A	H	G	S	V	T	236																							
hB7-H1	KTTT	T	N	S	K	R	E	E	K	F	N	M	T	S	T	L	R	I	N	T	T	N	E	I	F	Y	C	T	---	---	---	---	---	---	---	---	---	---	---	210																							
hB7-H2 long	PANT	S	H	S	R	T	P	E	G	Y	Q	V	T	S	V	L	R	L	K	P	P	P	R	N	F	S	V	---	---	---	---	---	---	---	---	---	---	---	---	193																							
hB7-H2 short	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	121																						
hB7IN prot	TSES	R	N	P	D	-	E	E	G	F	T	V	A	A	S	V	I	R	D	T	S	T	K	N	V	S	C	Y	I	Q	N	L	I	L	Q	E	K	K	V	E	I	S	P	A	S	S	L	P	R	L	T	P	245										
hB7IN2A1 prot	LKEV	S	M	P	D	-	A	D	G	F	M	V	T	T	A	V	---	I	R	D	K	S	V	R	N	M	S	C	S	I	N	N	T	L	L	Q	K	K	E	S	V	I	F	P	E	S	M	P	S	V	S	P	C	A	V	A	L	P	I	I	V	-	256
hB7IN2A2 prot	LKEV	S	I	A	D	-	A	D	G	F	M	V	T	T	A	V	---	I	R	D	K	Y	V	R	N	V	S	C	S	V	N	N	T	L	L	Q	E	K	E	T	V	I	F	P	E	S	M	P	S	A	S	P	W	M	V	A	L	V	I	L	T	A	261
hB7IN3A2 prot	VEAP	V	V	A	D	-	G	V	G	Y	E	V	A	A	S	V	I	R	G	G	S	C	E	G	V	S	C	T	I	R	N	S	L	L	G	L	E	K	T	A	S	I	S	A	D	P	E	R	S	---	---	---	---	---	---	---	---	---	---	245			
hB7I2.1 prot	LKEV	S	M	P	D	-	A	D	G	F	M	V	T	T	A	V	---	I	R	D	K	S	V	R	N	M	S	C	S	I	N	N	T	L	L	Q	K	K	E	S	V	I	F	P	E	S	M	P	S	V	S	P	---	---	---	---	---	---	---	---	247		
hB7I3.2 prot	VEAP	V	V	A	D	-	G	V	G	Y	E	V	A	A	S	V	I	R	G	G	S	C	E	G	V	S	C	T	I	R	N	S	L	L	G	L	E	K	T	A	S	I	S	A	D	P	E	R	S	---	---	---	---	---	---	---	---	---	---	245			
hB7I3.3 prot	VEGP	V	N	V	-	-	G	V	G	Y	A	V	P	P	P	V	I	---	I	T	S	G	G	E	V	S	C	I	I	T	N	S	L	L	G	L	E	K	T	A	S	I	S	A	D	P	E	I	Q	G	G	A	P	---	---	---	---	---	---	248			
hB7IN3A3 prot (hB7I3)	VEAP	V	V	A	D	-	G	V	G	Y	E	V	A	A	S	V	I	R	G	G	S	C	E	G	V	S	C	T	I	R	N	S	L	L	G	L	E	K	T	A	S	I	S	A	D	P	E	R	S	---	---	---	---	---	---	---	---	---	---	245			
hB7IN3A1 prot	VEAP	V	V	A	D	-	G	V	G	Y	E	V	A	A	S	V	I	R	G	G	S	C	E	G	V	S	C	T	I	R	N	S	L	L	G	L	E	K	T	A	S	I	S	A	D	P	E	R	S	---	---	---	---	---	---	---	---	---	---	245			
hB7I5 prot	VEAP	V	V	A	D	-	G	V	G	Y	E	V	A	A	S	V	I	R	G	G	S	C	E	G	V	S	C	T	I	R	N	S	L	L	G	L	E	K	T	A	S	I	S	A	D	P	E	R	S	---	---	---	---	---	---	---	---	---	---	245			
hB7.3	VEAP	V	V	A	D	-	G	V	G	Y	E	V	A	A	S	V	I	R	G	G	S	C	E	G	V	S	C	T	I	R	N	S	L	L	G	L	E	K	T	A	S	I	S	A	D	P	E	R	S	---	---	---	---	---	---	---	---	---	---	243			

FIG. 1B-1.

5/47

hB7-1	HLRV-NQT	-----	FNWNTTKQ	HFPDNL	PP	245
hB7-2	KTRLSSP	-----	FSIELED	QPPPDHI	---	240
hB7RP-1	-----	-----	-----	-----	---	235
hB7RP-2	-----	-----	-----	-----	---	236
hB7-H1	-----	-----	NHTA	LVIPEL	PLAHPN	240
hB7-H2 long	-----	-----	NTHV	RLTLAS	IDLQSQME	218
hB7-H2 short	-----	-----	-----	-----	PRTH	128
hB7IN prot	-----	-----	FRRLDP	-----	-----	284
hB7IN2A1 prot	-----	-----	-----	-----	-----	309
hB7IN2A2 prot	-----	-----	-----	-----	-----	310
hB7IN3A2 prot	-----	-----	-----	-----	-----	313
hB7I2 1 prot	-----	-----	-----	-----	-----	295
hB7I3 2 prot	-----	-----	-----	-----	-----	313
hB7I3 3 prot	-----	-----	-----	-----	-----	318
hB7IN3A3 prot (hB7I3)	-----	-----	-----	-----	-----	313
hB7IN3A1 prot	-----	-----	-----	-----	-----	313
hB7I5 prot	-----	-----	-----	-----	-----	313
hB7I3	-----	-----	-----	-----	-----	290

FIG. 1B-2.

6/47

hB7-1	-----	SWAITLISVNGIFVICCLTYCFAPCRER	-----	RRNERL	-----	280
hB7-2	-----	PMITAVLP	-----	TVIICVMVFCILWKWK	-----	274
hB7P-1	-----		-----		-----	241
hB7P-2	-----		-----		-----	236
hB7-H1	-----	LVI	-----	LGAILL	-----	250
hB7-H2 long	-----	PTM	-----	LLHIFIPSC	-----	230
hB7-H2 short	-----	PTM	-----	LLHIFIPSC	-----	140
hB1N prot	SK	ERLLEELK	-----		-----	299
hB1N2A1 prot	VK	EKLQEELR	RRTF	-----	-----	324
hB1N2A2 prot	-----	QQLQEELR	RRTF	-----	-----	323
hB1N3A2 prot	RKKSS	-----	-----	-----	-----	318
hB12.1 prot	VK	EKLQEELR	RRTF	-----	-----	310
hB13.2 prot	RKKIQYLTRGEES	-----	-----	-----	-----	326
hB13.3 prot	WRKIQYMARGEES	SSDTKKSALMLKWKKALFKPGDKMLQMRVSPCKINWMYSKIYCRKGELIKFISGRVK	-----	-----	-----	388
hB1N3A3 prot (hB73)	WRKIQYMARGEKSLAYHE	-----	-----	-----	-----	344
hB1N3A1 prot	WRSIQYASRGERHSAYNE	-----	-----	-----	-----	344
hB1F5 prot	WRSIQYASRGERHSAYNE	-----	-----	-----	-----	344
hB7.3	-----	-----	-----	-----	-----	290

FIG. 1B-3.

7/47

**FIG. 1C-1.**

8/47

h37-1	-----RRESVR	288
h37-2	-----ESEQTKKREIH	296
h37R-1	-----	262
h37R-2	-----	256
h37-HI	-----LRKG-----	264
h37-H2 long	-----LRKQL-----	247
h37-H2 short	-----LRKQL-----	157
h3IN prot	-----LHAVDVTLDPDTAHPHLFLYEDSKSVRLSDSR	331
h3IN2A1 prot	-----LHAVDVVLDPDTAHPDLFLSEDRRSVRRCPFR	356
h3IN2A2 prot	-----LHAADVVLDPDTAHPDLFLSEDRRSVRRGPYR	355
h3IN3A2 prot	-----LHAVDVVLDPDTAHPDLFLSEDRRSVRRCPFR	318
h3T2 1 prot	-----LHAVDVVLDPDTAHPDLFLSEDRRSVRRCPFR	342
h3T3 2 prot	-----NKSALMLK-----	338
h3T3 3 prot	-----GQARDTGFWKDLLSMAQALHAVALKSRKNGRPHGHLKL	528
h3IN3A3 prot (h3T3)	-----SAADVILYPDMANAIIIVSEDQRSVQRAEEP	368
h3IN3A1 prot	-----ANAIILLVSEDQRSVQRAEEP	345
h3T5 prot	-----ANPILLVSEDQRSVQRAKEP	368
h3T3 3	-----	290

FIG. 1C-2.



**FIG. 10-3.**

Alignment Report of hB/lineup, using Clustal method with PAM250 residue weight table.

hB7-1	-----PV	289
hB7-2	-----EAQRVFKSKTSSCDKSDTCF	323
hB7R-1	PETEL-----	298
hB7R-2	DQDGE-----	291
hB7-H1	CGIQDTNSKKQSDTHGE-----	289
hB7-H2 long	---DTTKPVTTKREVNSAI	274
hB7-H2 short	---DTTKPVTTKREVNSA	182
hB1N prot	LYNGG-YWALTPLRTPAGPPRRVGIFLDYESGDISFYNMNDGSDIYTFSNVTFSGPLRPFFCLWSSG	466
hB1N2A1 prot	MHKQ-Q-YAVSSPDRIIPKESLCRVGVFLDYEAGDVSYNMRDRSHIYTCPRSAFVPVR	485
hB1N2A2 prot	MFGNQ-YALSSPERIPKESLCRVGVFLDYEAGDVSYNMRDRSHIYTCPRSAFTVPVR	481
hB1N3A2 prot	-----	318
hB12.1 prot	MHKQ-Q-YAVSSPDRIIPKESLCRVGVFLDYEAGDVSYNMRDRSHIYTCPRSAFSGPDTSGSGDP	477
hB13.2 prot	-----	343
hB13.3 prot	LTDGNKYALTEPRTNKKPEPPRKVGIVLDYETGHISFYNATDGSHIYTFLHASSEPLYPVFRILTLE	665
hB1N3A3 prot (hB73)	LTDGNKYALTEPRTNKKPEPPRKVGIVLDYETGEISFYNATDGSHIYTFPHASFSEPLYPVFRILTLE	505
hB1N3A1 prot	-----MRH-----FVK	353
hB1F5 prot	LTDGNKYALTEPRTNKKPKPKKVGIVLDYETGDISFYNAVDSGSHIHTFLDVSFSEALYPVFRILTLE	504
hB7.3	-----	290

FIG. 1D-1.

hB7-1	-----TESWNLL-----	289
hB7-2	-----GEGSKTA-----	323
hB7P-1	-----GEGSKTA-----	306
hB7P-2	-----GEGSKTA-----	312
hB7-H1	-----GEGSKTA-----	289
hB7-H2 long	-----GEGSKTA-----	274
hB7-H2 short	-----GEGSKTA-----	182
hB1N prot	KKPLTICIAADGPERVTVIANAQDLSKEIPSSDMGEESAPRDADTLHSKLIPTQPSQGAP,	527
hB1N2A1 prot	-----FFRLGCEDSPIFICPALTG--ANGVT---VPEEGLTLH-RVG---THQSL,	528
hB1N2A2 prot	-----FFRLGSDDSPIFICPALTG--ASGVM---VPEEGLKLH-RVG---THQSL,	524
hB1N2A2 prot	-----FFRLGSDDSPIFICPALTG--ASGVM---VPEEGLKLH-RVG---THQSL,	318
hB1N2A2 prot	PEPIESIWSHSHVDKPWSFQQPPHNTHLPAAAF-----TPTTDLSPSFLLL---TRLCF,	530
hB12.1 prot	-----KKG-----EEM	350
hB13.2 prot	PTALTVCIPK-VESSPDSDLVPDHSLEIPITGLANESGEPQAEVTSLLPAQPGAKGLTLHNSQSEP,	734
hB13.3 prot	PTALTVCIPKEVESSPDSDLVPDHSLEIPITGLANESGEPQAEVTSLLPAHPGAEVSPSATTNQNHK	575
hB1N2A3 prot (hB73)	PTALTVCIPKEVESSPDSDLVPDHSLEIPITGLANESGEPQAEVTSLLPAHPGAEVSPSATTNQNHK	353
hB1N2A1 prot	PTALSICPA.	514
hB1F5 prot	-----	290
hB7.3	-----	

FIG. 1D-2.

hb7-1	-----LLS	289
hb7-2	-----QEIA.	323
hb7RP-1	-----T	309
hb7RP-2	-----T	317
hb7-HI	-----T	290
hb7-H2 long	-----I	274
hb7-H2 short	-----I	183
hbIN prot		527
hbIN2A1 prot		528
hbIN2A2 prot	-----T.	524
hbIN3A2 prot	-----T.	320
hb72.1 prot	LQMRLHLVK.	530
hb73.2 prot		360
hb73.3 prot		734
hbIN3A3 prot (hb73)	LQARTEALY.	585
hbIN3A1 prot		353
hb7F5 prot	-----M	514
hb7.3	-----M	291

FIG. 1D-3.

**FIG. 2A.**

hB7-H2	long	DRF	570
hB7-H2	short	DRF	361
hB7-H1	orf		621
hB7-H2	long	DRF	638
hB7-H2	short	DRF	368
hB7-H1	orf		685
hB7-H2	long	DRF	707
hB7-H2	short	DRF	437
hB7-H1	orf		755
hB7-H2	long	DRF	776
hB7-H2	short	DRF	506
hB7-H1	orf		825
hB7-H2	long	DRF	822
hB7-H2	short	DRF	552
hB7-H1	orf		873

Decoration 'Decoration #1': Shade (with dots) residues that match hB7-H1 orf exactly.

**FIG. 2B.**

hB7-H1 orf vs hB7-H2 long orf

GAP of : hB7-H1 orf from: 1 to: 873 to: hB7-H2 long orf from: 1 to: 822

Percent Similarity: 58.312 Percent Identity: 58.312

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      .       .       .       .
1  ATGAGGATATTGCTGTCTTTATATT...CATGACCTACTGGCATTGCT  47
      | ||| ||      | | || ||      | ||      | ||| |
1  ...ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCA  47
      .       .       .       .
48  GAACGC.....ATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAG  91
      || ||      ||| || || || || || || || || || || ||
48  GATAGCAGCTTTATTCACAGTGACAGTCCCTAAGGAAGTGTACATAATAG  97
      .       .       .       .
92  AGTATGGTAGCAATATGACAATTGAATGCAAATCCCAGTAGAAAAACAA 141
      || |||| |||| |||| | |||| |||| ||      | || ||
98  AGCATGGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCAT 147
      .       .       .       .
142 TTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACAT 191
      | |||| | ||| ||| | | || | ||| || | ||| ||
148 GTGAACCTTGAGCAATAACAGCCAGTTTGCAAAAGGTG....GAAAAT 192
      .       .       .       .
192 TATTCAATTGTGTCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCT 241
      || ||      || ||      || ||
193 GATACA.....TCCCCA.....C 205
      .       .       .       .
242 ACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCT 291
      || | | || ||| || || || || || || || || || || ||
206 ACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCTAGGGAAGGCC 255
      .       .       .       .
292 GCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTG 341
      | | || || | | || || || || || || || || || || ||
256 TCGTTCCACATAGCTCAAGTCCAAGTGAGGGACGAAGGACAGTACCAATG 305
      .       .       .       .
342 CATGATCAGCTATGGTGGTGCC...GACTACAAGCGAATTACTGTGAAAG 388
      ||| |||| |||| || ||| |||| |||| || ||| |||||
306 CATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAG 355
      .       .       .       .

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FIG. 3A.

16/47

389 TCAATGCCCCATACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCA 438  
| | | | | | | | | | | | | | | | | | | | | |  
356 TCAAAGCTTCCTACAGGAAAATAAAC. . . ACTCACATCCTAAAGGTTCCA 402  
| | | | | | | | | | | | | | | | | | | | | |  
439 GTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGC 488  
| | | | | | | | | | | | | | | | | | | | | |  
403 GAAACAGATGAGGTAGAGCTCACCTGCCAGGCTACAGGTTATCCTCTGGC 452  
| | | | | | | | | | | | | | | | | | | | | |  
489 CGAAGTCATCTGGACAAGCAGTGACCATCAAGTCCTGAGTGGTAAGACCA 538  
| | | | | | | | | | | | | | | | | | | | | |  
453 AGAAGTATCCTGGCCAAAC. GTCAGCGT. . . TCCTG. . . . . CCA 487  
| | | | | | | | | | | | | | | | | | | | | |  
539 CCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCAC 588  
| | | | | | | | | | | | | | | | | | | | | |  
488 ACACCAGCCACTCCAGGACCCCTGAAGGCCTCTACCAGGTCACCAGTGTT 537  
| | | | | | | | | | | | | | | | | | | | | |  
589 CTGAGAATCAACACAACAACTAATGAGATTTTCTACTGCATTTTAGGAG 638  
| | | | | | | | | | | | | | | | | | | | | |  
538 CTGCGCCTAAAGCCACCCCTGGCAGAACTTCAGCTGTGTGTTCTGGA. 586  
| | | | | | | | | | | | | | | | | | | | | |  
639 ATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTAC 688  
| | | | | | | | | | | | | | | | | | | | | |  
587 ATACTCACGTGAGGGAA. . CTTAC. . . . . TTTGGCCAGCATTGACCT. T 627  
| | | | | | | | | | | | | | | | | | | | | |  
689 CTCTGGCACATCCTCCAAATGAAAGGACTCACTGG. TAATTCTGGGAGC 737  
| | | | | | | | | | | | | | | | | | | | | |  
628 CAAAGTCAGATGGAACCCAGGACCCATCCAACCTTGGCTGCTTCACATTT 677  
| | | | | | | | | | | | | | | | | | | | | |  
738 CATCTTATTATGCCTTGGTG. TAGCACTGACATTTCATCTTCCGTTTAAGA 786  
| | | | | | | | | | | | | | | | | | | | | |  
678 CATCCCCTCCTGCATCATTGCTTTTCAATTTTCAT. . AGCCACAGTGATAGC 725  
| | | | | | | | | | | | | | | | | | | | | |  
787 AAAGGGAGAATGATGGATGTGAAAAAATGTGGCATCCAAGATACAAACTC 836  
| | | | | | | | | | | | | | | | | | | | | |  
726 CCTAAGA. AAACAACCTCTGTCAAAGCTGTATTCTTCAAAGACACA. AC 773  
| | | | | | | | | | | | | | | | | | | | | |  
837 AAAGAAGCAAAGTGATACACATTTGGAGGAGACGTAA. . . . . 873  
| | | | | | | | | | | | | | | | | | | | | |  
774 AAA. AAGACCTGTCA. CCACAACAAAGAGGGAAGTGAACAGTGCTATCTG 821  
:  
:

FIG. 3B.



17/47

hB7-H1 orf vs hB7-H2 short orf

GAP of : hB7-H1 orf from: 1 to: 873 to: hB7-H2 short orf from: 1 to: 552  
Percent Similarity: 59.811 Percent Indentity: 59.811

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      .               .               .
1  ATGAGGATATTTGCTGTCTTTATATT...CATGACCTACTGGCATTGCT  47
      | ||| ||      | | || ||      ||      || | |
1  ...ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCA  47
      .               .               .
48 GAACGC.....ATTACTGTACGGTTCCCAAGGACCTATATGTGGTAG  91
      || ||      ||| || || || || || || || || || || ||
48 GATAGCAGCTTTATTCACAGTGACAGTCCCTAAGGAAGTGTACATAATAG  97
      .               .               .
92 AGTATGGTAGCAATATGACAATTGAATGCAAATCCCAGTAGAAAAACAA 141
      || |||| |||| || || | |||| || ||      | || ||
98 AGCATGGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCAT 147
      .               .               .
142 TTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACA 191
      | |||| | ||| || | | | || || ||      ||| ||
148 GTGAACCTTGGAGCAATAACAGCCAGTTTGCAAAGGTG....GAAAT 192
      .               .               .
192 TATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCT 241
      || ||      || ||
193 GATACA.....TCCCA.....C 205
      .               .               .
242 ACAGACAGAGGGCCCGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCT 291
      || | | || || || || || || || || || || || || ||
206 ACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCCTAGGGAAGGCC 255
      .               .               .
292 GCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTG 341
      | | || || | | || || || || || || || || || ||
256 TCGTTCCACATACCTCAAGTCCAAGTGAGGGACGAAGGACGTACCAATG 305
      .               .               .
342 CATGATCAGCTATGGTGGTGCC..GACTACAAGCGAATTACTGTGAAAG 388
      ||| |||| |||| | || | |||| || || || || || ||
306 CATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAG 355
      .               .               .

```

FIG. 4A.

18/47

```
389 TC. AATGCCCCATACAACAAAATCAACCAAAGAATTTTGGTTGTGGA... 434
    || || | | || || | | || | | | | |
356 TCAAAGGTCAGATGGAAC. CCAGGACCCATCCAACCTGGCTGCTTCACAT 404
    . TCCAGTCACCTCTGAACATGAACTGACATGT... CAGGCTGAGGGCTAC 480
    | || | | || | | || | | || | || |
405 TTTTCATCCCCTCCTGCATCATTGCTTTTCATTTTCATAGCCACAGTGATAG 454
    . CCCAAGGCCGAAGTCATCTG. GACAAGCAGTGACCATC. AAGTCCTGAGT 528
    ||| | | || ||| | ||| || | || | |
455 CCCTAAG. AAAACAACCTCTGTCAAAGCTGTATTCTTCAAAGACACAAC 503
    GGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGT 578
    |||| | |||| | |||| | || | || |
504 AAAAAGAC. . CTGTCACCACAACAAGAGGGAAGTGAA. CAGTGCTATCT 550
    GACCAGCACACTGAGAATCAACACAACAATAATGAGATTTTCTACTGCA 628
    ||
551 GA..... 552
```

FIG. 4B.

19/47

hB7-H2 long vs hB7-H1

GAP of: hB7-H2 long aa from: 1 to: 273 to: hB7-H1 aa from: 1 to: 290

Percent Similarity: 46.792 Percent Identity: 37.358

```
1 MIFLLMLSLELQLHQIAALFTVTPKELYIIHGNSVTLECNFDTGSHV 50
      : : : : : |||||:|:|:|:|:|:|:|:|
1 ..MRIFAVFIFMTYWHLLNAFTVTPKDLVVEYGSNMTIECKFPVEKQL 48

51 NLGAITASLQKVENDT.....SPHRERATLLEEQLPLGKAS 86
      .| |: : : : | :|:| |:|:| |:|
49 DLAALIVYWEMEDKNIIQFVHGEECLKVQHSSYRQRARLLKDQLSLGNAA 98

87 FHIPQVQVRDEGQYQCIIYGVAWDYKYLTLKVKASYRKINTHILKV. PE 135
      | |...| | |.| || | ||:|.|| | | || | || |
99 LQITDVKLQDAGVYRCMISYGGA. DYKRITVKVNAPYNKINQRILVDPV 147

136 TDEVELTCQATGYPLAEVSWPN....VSPANTSHSRTPEGLYQVTSVL 180
      | | ||||| ||| ||| | . | |...| |:|:| |||
148 TSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTL 197

181 RLKPPPGRNFSCVF....WNTHVRELTLASIDLQSQMEPRTHPTWLLHI 225
      |: | | | | | : | : | | | :|
198 RINTTTNEIFYCTFRRLDPEENHTAELVIPELPLAHPNERTHLV. ILGA 246

226 FIPSCIIAFIFIATVIALRKQLCQKLYSSKDTTKRPVTTTKREVNSAI 273
      : :| || . | .| .|: | |
247 ILLCLGVALTFIFRLRKGRMMDVKKCGIQDTNSKKQSDTHLEET.... 290
```

FIG. 5.

20/47

hB7-H2 short vs hB7-H1  
GAP of : hB7-H2 short aa from: 1 to: 183 to: hB7-H1 aa from: 1 to: 290  
Percent Similarity: 41.243 Percent Identity: 28.249

```

1  MIFLLLMLSLELQLHQIAALFTVTPKELYIEHGSNVTLECNFDTGSHV  50
      : . . . : | | | | | : | : | : | | . | : | |
1  ..MRIFAVFIFMTYWHLNNAFTVTPKDLVVVEYGSNMTIECKFPVEKQL  48
      : . . . : . . . . . . . . . . . . . . . . . .
51 NLGAITASLQKVENDT.....SPHRERATLLEEQLPLGKAS  86
      . | | : . . . . . . . . . . . . . . . . . .
49 DLAALIVYWEMEDKNIIQFVHGEEDLKVQHSSYRQRARLLKQSLGNAA  98
      : . . . | | . | . | | | | | | : | . | | | |
87 FHIPQVQVRDEGQYQCIIYGVAWDYKYLTLKVKGQMEPRTHPTWLLHIF 136
      | | . . | | | . | | | | | | | : | . | | | |
99 LQITDVKLQDAGVYRCMISYGGA. DYKRITVKVNA...PYNKINQRILVV 144
      : . . . : . . . . . . . . . . . . . . . . .
137 IPSCIIAFIFIATVIALRKQLCQKLYSSKDTTKRPVTTTKREVNSAI... 183
      | : . . . : . . . . . . . . . . . . . . .
145 DPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVT 194

```

⋮

FIG. 6.

21/47

hB7-H2 long orf vs hB7-H2 short orf

GAP of: hB7-H2 long orf from: 1 to: 822 to: hB7-H2 short orf from: 1 to: 552

Percent Similarity: 100.000 Percent Identity: 100.000

```

      .           .           .           .
1  ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGAT  50
   ||||||||||||||||||||||||||||||||||||||||||||||||
1  ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGAT  50

      .           .           .           .
51 AGCAGCTTTATTACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGC 100
   ||||||||||||||||||||||||||||||||||||||||||||||||
51 AGCAGCTTTATTACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGC 100

      .           .           .           .
101 ATGGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCATGTG 150
   ||||||||||||||||||||||||||||||||||||||||||||||||
101 ATGGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCATGTG 150

      .           .           .           .
151 AACCTTGGAGCAATAACAGCCAGTTTGCAAAGGTGGAAAATGATACATC 200
   ||||||||||||||||||||||||||||||||||||||||||||||||
151 AACCTTGGAGCAATAACAGCCAGTTTGCAAAGGTGGAAAATGATACATC 200

      .           .           .           .
201 CCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCCTAGGGA 250
   ||||||||||||||||||||||||||||||||||||||||||||||||
201 CCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCCTAGGGA 250

      .           .           .           .
251 AGGCCTCGTTCCACATACCTCAAGTCCAAGTGAGGGACGAAGGACAGTAC 300
   ||||||||||||||||||||||||||||||||||||||||||||||||
251 AGGCCTCGTTCCACATACCTCAAGTCCAAGTGAGGGACGAAGGACAGTAC 300

      .           .           .           .
301 CAATGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCT 350
   ||||||||||||||||||||||||||||||||||||||||||||||||
301 CAATGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCT 350

      .           .           .           .
351 GAAAGTCAAAGCTTCCTACAGGAAAATAAACACTCACATCCTAAAGGTTC 400
   |||||||||||
351 GAAAGTCAAAG..... 361

```

FIG. 7A.

22/47

:

601 GAACTTACTTTGGCCAGCATTGACCTTCAAAGTCAGATGGAACCCAGGAC 650  
|||||  
362 ..... GTCAGATGGAACCCAGGAC 380

651 CCATCCAACCTGGCTGCTTACATTTTCATCCCCTCCTGCATCATTGCTT 700  
|||||  
381 CCATCCAACCTGGCTGCTTACATTTTCATCCCCTCCTGCATCATTGCTT 430

701 TCATTTTCATAGCCACAGTGATAGCCCTAAGAAAACAACTCTGTCAAAG 750  
|||||  
431 TCATTTTCATAGCCACAGTGATAGCCCTAAGAAAACAACTCTGTCAAAG 480

751 CTGTATTCTTCAAAGACACAACAAAAGACCTGTCACCACAACAAAGAG 800  
|||||  
481 CTGTATTCTTCAAAGACACAACAAAAGACCTGTCACCACAACAAAGAG 530

801 GGAAGTGAACAGTGCTATCTGA 822  
|||||  
531 GGAAGTGAACAGTGCTATCTGA 552

FIG. 7B.

23/47

hB7-H2 long vs hB7-H2 short

GAP of: hB7-H2 long aa from: 1 to: 273 to: hB7-H2 short aa from: 1 to: 183  
Percent Similarity: 74.444 Percent Identity: 71.667

```

      . . . . .
1  MIFLLLMLSLELQLHQIAALFTVTPKELYIIHGNSVTLECNFDTGSHV  50
   ||||||||||||||||||||||||||||||||||||||||||||
1  MIFLLLMLSLELQLHQIAALFTVTPKELYIIHGNSVTLECNFDTGSHV  50

      . . . . .
51 NLGAITASLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQY 100
   ||||||||||||||||||||||||||||||||||||||||||||
51 NLGAITASLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQY 100

      . . . . .
101 QCIIIYGVAWDYKYLTLKVKASY. . RKINTHILKV. PETDEVELTCQATG 147
     |||||||||||||||| | | : | : . : ||
101 QCIIIYGVAWDYKYLTLKVKQMEPRTHPTWLLHIFIPSCIIAFIFIATV 150

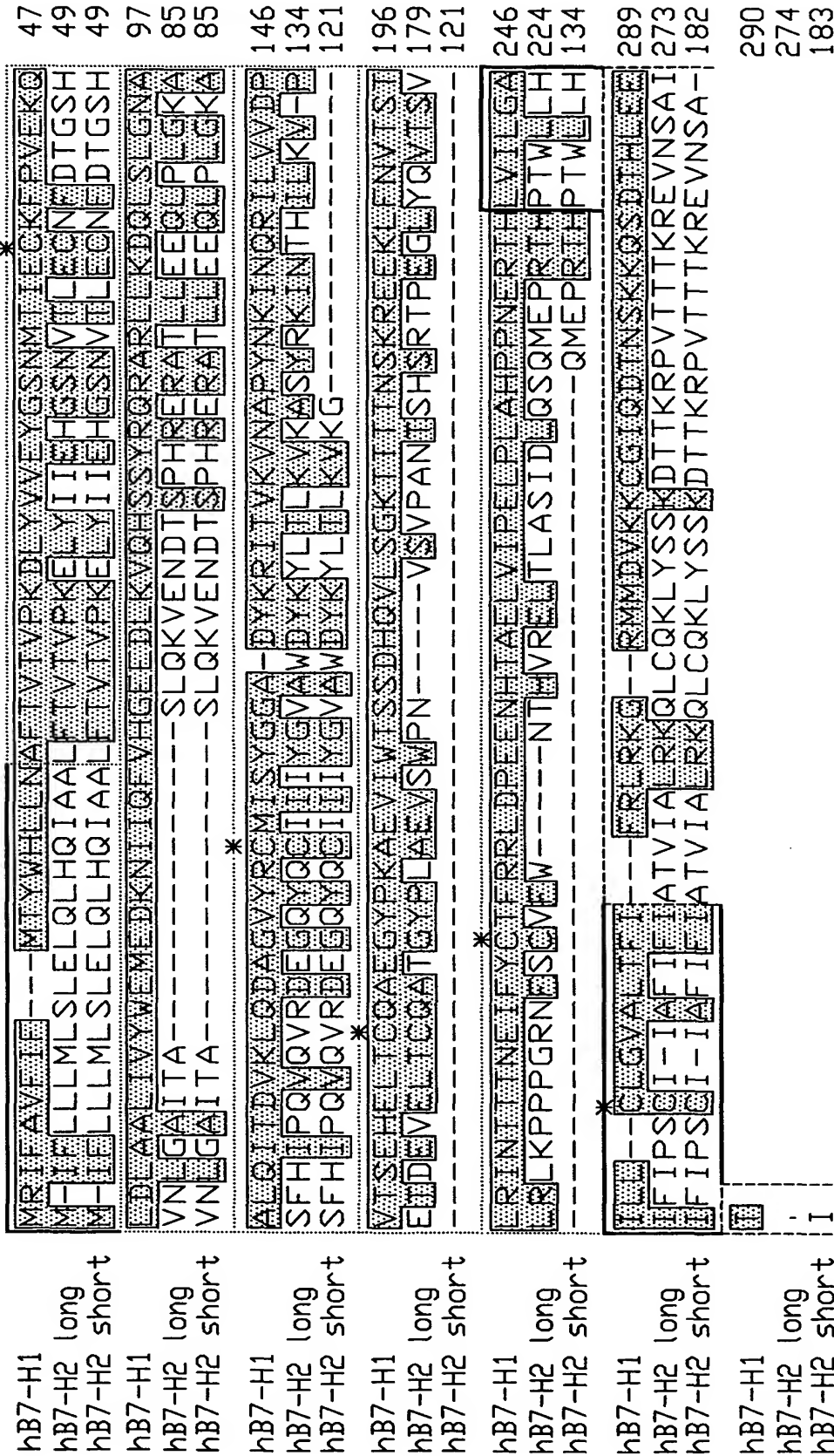
      . . . . .
148 YPLAEVSWPNVSPANTSHSRTPEGLYQVTSVLRLKPPPGRNFSCVFWNT 197
     | . . . . | . : | | :
151 IALRKQLCQKLYSSKDTTKRPVTTTKREVNSAI..... 183

```

⋮

**FIG. 8.**

24/47



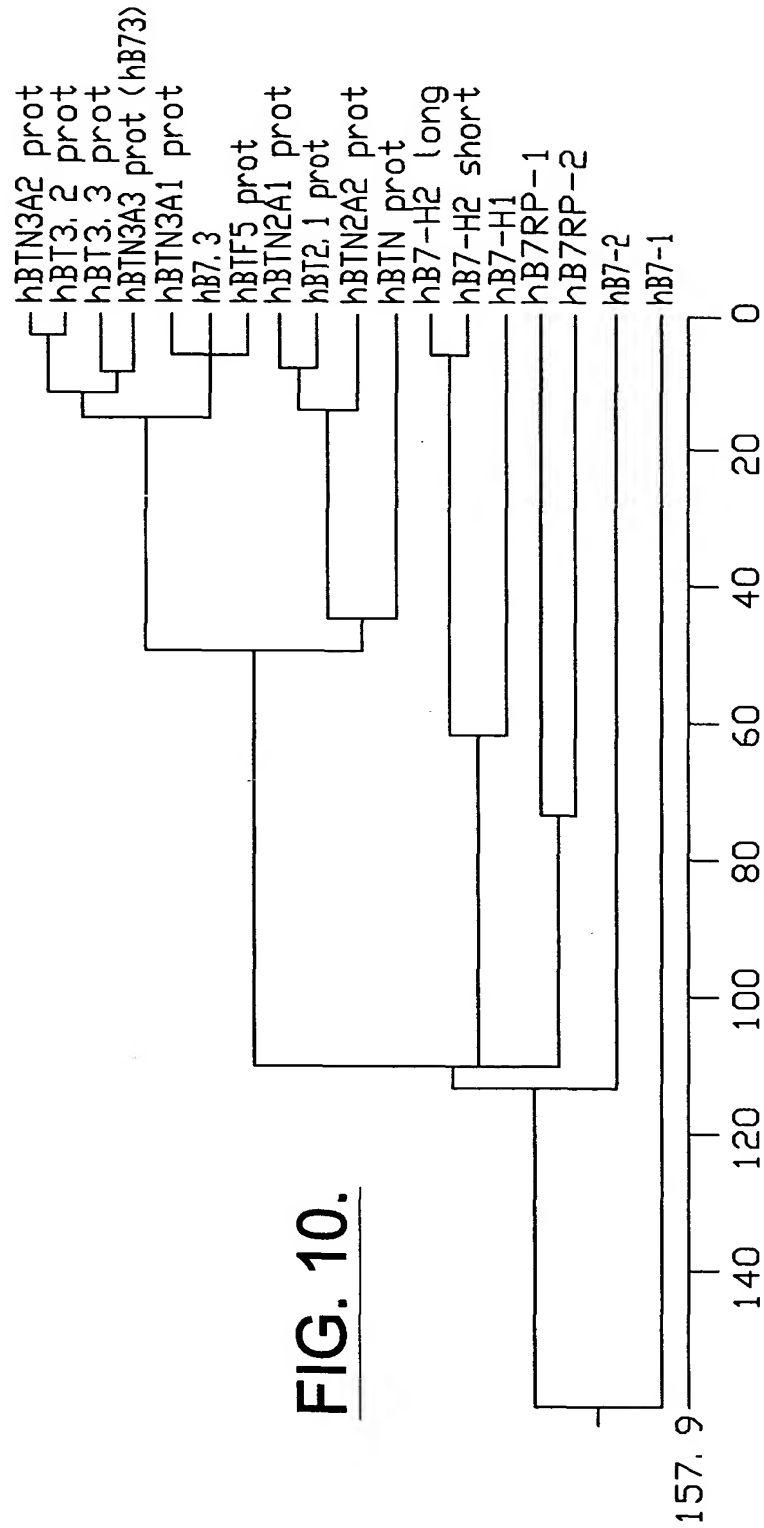
Decoration 'Decoration #1: Shade (with dots) residues that match hB7-H1 exactly.



FIG. 9.



25/47



Alignment Report of hb71.nup, using Clustal method with PAM250 residue weight table.

Alignment Report of hb7/lineup, using Clustal method with PAM250 residue weight table.	
66	hb7-1
51	hb7-2
54	hb7RP-1
67	hb7RP-2
57	hb7-H1
57	hb7-H2 long
57	hb7-H2 short
126	hb7-1
114	hb7-2
122	hb7RP-1
130	hb7RP-2
123	hb7-H1
112	hb7-H2 long
112	hb7-H2 short
188	hb7-1
182	hb7-2
184	hb7RP-1
191	hb7RP-2
180	hb7-H1
163	hb7-H2 long
121	hb7-H2 short
249	hb7-1
244	hb7-2
248	hb7RP-1
243	hb7RP-2
236	hb7-H1
214	hb7-H2 long
124	hb7-H2 short

27/47

hB7-1	TLISVNGIFV	CC	TY	FAPRCRERRRNERL	---	RR	SVR	---	286
hB7-2	AVLP	---	TVI	CVMVF	---	WKWKKKRPRNSYK	GTNTMEREESEQTKKR	KIHIPERSDEAQRVFKSS	311
hB7RP-1	TGEKNATWS	LAV	---	LC	LV	---	VVAVAIGMVC	DRCLQHSYAGAWAVSP	306
hB7RP-2	FPPE	---	ALW	TVGS	SV	---	LI	VALAFVCMRKIKQSC	305
hB7-H1	ER	LV	GG	AL	---	CGV	---	FR	278
hB7-H2 long	PR	HT	WL	HL	---	IP	SC	I	262
hB7-H2 short	PR	HT	WL	HL	---	IP	SC	I	172
hB7-1	---	---	PV	---	---	---	---	---	289
hB7-2	K	SS	CD	K	SD	TCF	---	---	323
hB7RP-1	---	---	---	---	---	LLS	---	---	309
hB7RP-2	DSKED	---	GG	Q	E	IA	---	---	317
hB7-H1	SKKQS	---	TH	L	E	E	---	---	290
hB7-H2 long	---	---	---	---	---	---	---	---	274
hB7-H2 short	---	---	---	---	---	---	---	---	183

Decoration 'Decoration #1': Shade (with dots) residues that match the Consensus exactly.

FIG. 11B.

28/47

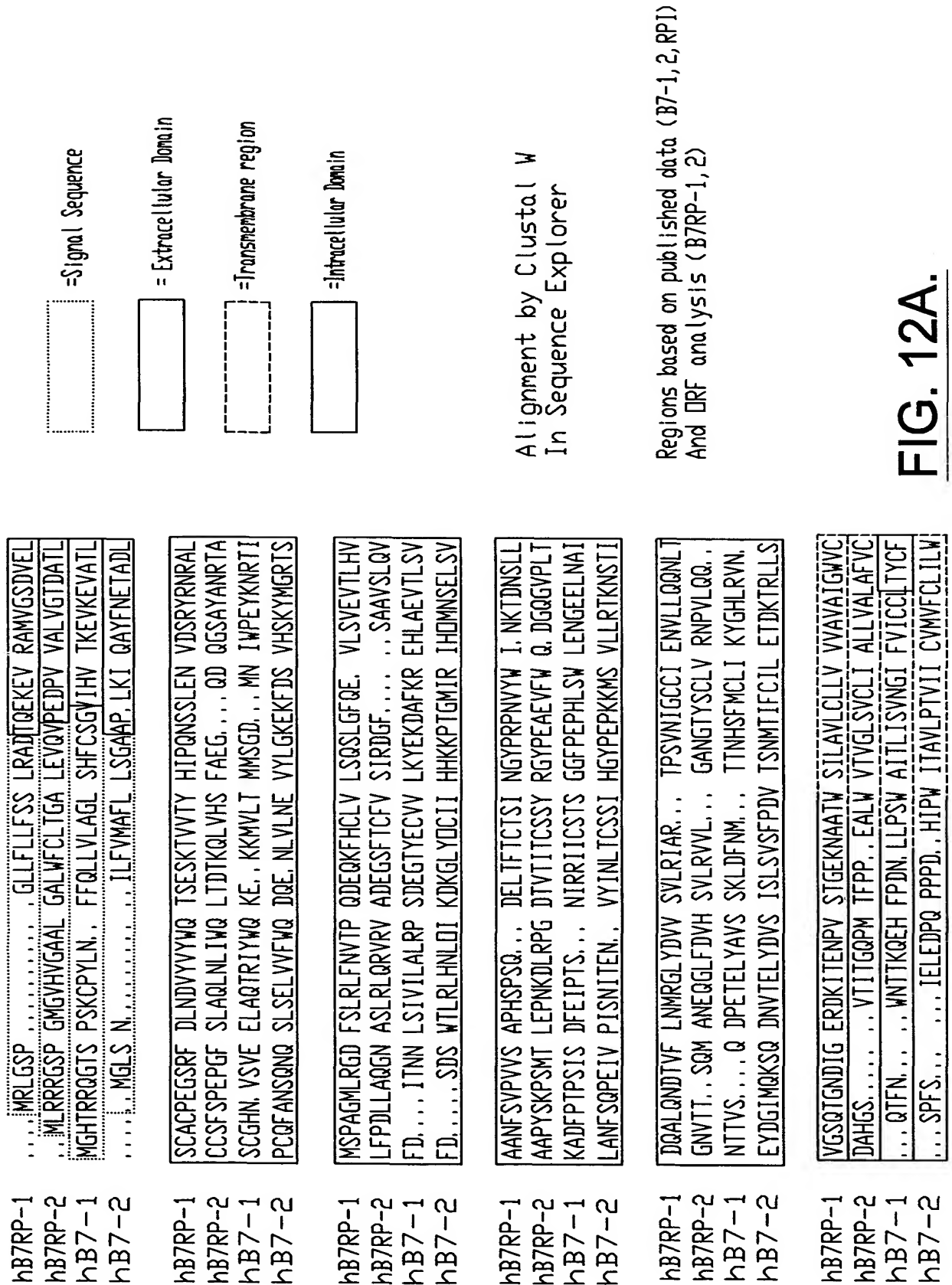


FIG. 12A.

29/47

hB7RP-1	RDRCLQHS, Y AGAWAVSPET ELTGHV.....
hB7RP-2	WRKIKQSCEE ENAGAEQDQG EGECSKTALQ PLKHSDSKED DGQEIA....
hB7-1	APRCRERRRN ERLRESVRP V.....
hB7-2	KWKKKRPRN SYKCGTNTME REESEQTKKR EKIHIPERSD EAQRVFKSSK
hB7RP-1	.....
hB7RP-2	.....
hB7-1	.....
hB7-2	TSSCDKSDIC F

FIG. 12B.

[illegible]

Decoration 'Decoration #1: Shade residues that match the Consensus exactly.

**FIG. 13B.**

32/47

# hB7RP-2 vs hB7-1

Gap of: hB7RP-2 aa from: 1 to: 316 to: hB7-1 aa from: 1 to: 288

Percent Similarity: 32.734 Percent Identity: 24.820

```

1  ..MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATL 48
      ||.||.          |  |  |          |  |  |||
1  MGHTRRQGTSPSKCPYLNFFQLL..VLAGLSHFCSGVIHVTKEVKEVATL 48

49  CCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPD 98
      | .      ||| : || : | .. .      | |||
49  SCGHNVSV.E.LAQTRIYWQ.KEKKMVLTMMSGDMNIWPEYKNRTIFD.. 94

99  LLAQGNASRLRQVRVADEGSFTCFV.....SIRDFGSAAVSLQVAAPY 142
      | |: : .| .|||: | | . :      | |. | | :
95  ..ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTL SVKADF 142

143 SKPSMTLEPNKDLRPGDTVITITCSSYRGYPEAEVFWQDGGQVPLTGNVTT 192
      ||.. . : : . | ||. ||| . | : | | ||
143 PTPSIS...DFEIPTSNIRRIICSTSGGFPEPHLSWLE.NGEELNAINTT 188

193 SQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPNVLQQDAHGSVTITGQPM 242
      | |: | | | : | : : |||: | . . . | |
189 VSQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHRLRVNQTFNWNTTKQE. 237

243 TFPPEAL..WVTVGLSVCLIALLVAFVCWRKIKQSCEEENAGAEDQDG 290
      || | | | : || | : | : : : | |
238 HFPDNLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRP 287

291 EGEKSKTALQPLKHSDSKEDDGQEIA 316

288 V..... 288

```

**FIG. 14.**





34/47

hB7RP-1 vs hB7-2

Gap of: hB7RP-1 aa from: 1 to: 302 to: hB7-2 aa from: 1 to: 323

Percent Similarity: 31.250 Percent Identity: 21.181

```

      .       .       .       .
1  MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDV  50
      :|  :||: . | .       .:|  :|  |  :|
1  ..MGLSNILFVM. AFLLSGAAPLKIQAYFNETADLPCQFANSQNQSLSEL  47

      .       .       .       .
51  YVYWQTSESKTVVTYHIPQNSSLENVDSRYRNRALMSPAGMLRGDFSLRL 100
      |:|  .| .       :| .       :| |  |  .:|
48  VVFWQDQENLVLNEVYL GK. EKFD SVHSKYMGR TSFD. .... SDSWTLRL  91

      .       .       .       .
101 FNVTPQDEQKFHCLV. LSQSLGFQEVLSVEVTLHVAANF SVP. VVSAPH S 148
      | .  .| .  :|: .  |  : .  | | | | |  :| .
92  HNLQIKDKGLYQCI IHHKKPTGMIRI HQMNSELSVL ANFSQPEIVPISNI 141

      .       .       .       .
149 PSQDEL TFTCTSINGYPRP. NVYWINKTDNSLLDQALQNDTVFLNMRGLY 197
      :  ||. ||. || |  .  : :| || :|  .  |  ||
142 TENVYINLTCSSIHGYPEPKMSVLLRTKNSTIEYDGIMQKSQDNVTELY 191

      .       .       .       .
198 DVVSVLRIARTPSVNIGCC IENVLLQQNLTVGSQTGNDIGERDKITENPV 247
      ||  | :  | |  |  :| .  | .  | .  :
192 DVSISLSVS. FPDVTSNMTIFCILETDKTRLLSSPF SIELED PQPPPDHI 240

      .       .       .       .
248 STGEKNAATWSILAVLC LLVVVAIGA WVC RDRCLQHSYAGAWAVSPETE 297
      |  .  :|: |  :  |  : |  |  .  |
241 PWITAVLPT. ... VIICVMVFCLILWKWKKKRPRNSYKCGTNTMEREES 286

      .
298 LTGHV..... 302

      .
287 EQTKKREKIHIPERSDEAQRVFKSSKTSSCDKSDTCF 323
```

**FIG. 16.**

35/47

hB7RP-1 vs hB7-1

Gap of: hB7RP-1 aa from: 1 to: 302 to: hB7-1 aa from: 1 to: 288

Percent Similarity: 30.292 Percent Identity: 24.088

```

      .           .           .           .
1  .....MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDELSC 37
      .           .           .           .
1  MGHTRRQGTSPSKCPYLNFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSC 50
      .           .           .           .
38  ACPEGSRFDLNDVYVYWQTSESKTVVTYHIPQNSSLENVDJSRYRNRALMS 87
      .           .           .           .
51  G. HNVSVEELAQTRIYWQ. KKKMVL... MMSGDMNIWPEYKNRTIFD 94
      .           .           .           .
88  PAGMLRGDFSLRLFNVTPQDEQKFHCLVLS. QSLGFQEVLSVEVTLHVAA 136
      .           .           .           .
95  ....ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKA 140
      .           .           .           .
137 NFSVPVVSAPHSPSQDELFTCTTSINGYPRPNVYWINKTDNSLLDQALQN 186
      .           .           .           .
141 DFPTPSISDFEIPTSNIRRIICSTSGGFPEPHLSWL... ENGEELNAINT 187
      .           .           .           .
187 DTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENTVLLQQNLTVGSQTGNDI 236
      .           .           .           .
188 TVSQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHRLVNQTFNWNTTKQE 237
      .           .           .           .
237 GERDKITENPVSTGEKNAATWSILAVLCLLVVVAIGAIGWVCRDRCLQHSY 286
      .           .           .           .
238 HFPDNLPSWAIT... LISVNGIFVICCLTYCFAPRCRERRRNERLRRES 284
      .
287 AGAWAVSPETELTGHV 302
      .
285 VRPV..... 288
```

FIG. 17.

36/47

hB7RP-1 vs hB7RP-2

Gap of: hB7RP-1 aa from: 1 to: 302 to: hB7RP-2 aa from: 1 to: 316

Percent Similarity: 35.842 Percent Identity: 30.824

```

1 .....MRLGSPGLLFLFSSLRADTQEKEVRAMVGSDVELSC 37
      .      | | | . |      | | | | | | | |
1 MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDLCC 50
      .      | | . . | | . . | .      . . | | | | :
38 ACPEGSRFDLNDVYVYWQTSKTVVTYHIPQNSSLENVDSRYRNRALMS 87
      .      | | . . | | . . | .      . . | | | | :
51 SFSPEPGFSLAQLNLIWQLTDKQLV. . . HSFAEGQDQGSAYANRTALF 96
      | : . | . | | | | | | | | | | . | | | | |
88 PAGMLRGDFSLRLFNVTPQDEQKFHCLVLSQSLGFQEVLSVEVTLHVAAN 137
      | : . | . | | | | | | | | | | . | | | | |
97 PDLLAQGNASRLQRVRVADEGSFTCFVSIRDFG. . . . SAAVSLQVAAP 141
      .      | | | | | | | | | | | | | | | | | |
138 FSVPPVVSAPHSPS. . QDELTFTCTSINGYPRPNVYWINKTDNSLLDQAL 184
      : | | | . . . | . | | | | | | | | | | |
142 YSKPSMTLEPNKDLRPGDVTITCSSYRGYPEAEVFWQDGGGVPLTGNVT 191
      .      | | | | | | | | | | | | | | | | | |
185 QNDTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQTGN 234
      .      | | | | | | | | | | | | | | | | | |
192 TSQ. . MANEQGLFDVHSLRVVLGANGTYSLVRNPVLQQD. AHGSVT. . 236
      .      | | | | | | | | | | | | | | | | | |
235 DIGERDKITENPVSTGEKNAATWSILAVLCLLVVVAVAIGWVCRDRCLQH 284
      | | | | . . . | | . . | : . | | : . | | : |
237 .....ITGQPMTFPPE. . ALWVTVGLSVCLIALLLVALAFVCWRKIKQS 277
      .      | | | | | | | | | | | | | | | | | |
285 . SYAGAWAVSPETELTGHV. . . . . . . . . . . . . . . 302
      | | : | | |
278 CEEENAGAEDQDGEGEKSKTALQPLKHSDSKEDDGQEIA 316

```

**FIG. 18.**

37/47

# hB7-1 vs hB7-2

Gap of: hB7-1 aa from: 1 to: 288 to: hB7-2 aa from: 1 to: 323

Percent Similarity: 33.579 Percent Identity: 22.878

```

      .           .           .           .
1  MGHTRRQGTSPSKCPYLNFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSC 50
      :           :| .           : :           ||||
1  ..... MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPC 34
      .           .           .           .
51  GH. NVSVEELAQTRIYWQKEKKMVLTM. ... SGDMNIWPEYKNRTIFDI 95
      | : | : :|| : : || .           : : | |||
35  QFANSQNQSLSELVFWQDQENLVNEVYLGKEKFDVHSKYMGRTSFD. 83
      .           .           .           .
96  TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPTP 145
      ... : : | . | . | :|| : .           | | ||| | . |
84  SDSWTLRLHNLQIKDKGLYQCIIHKKPTGMIRIHQMNSELSVLNFSQP 133
      .           .           .           .
146  SISDFEIPTSNIR. RIICSTSGGFPEPHLSWLENGEELNAIN. ... TTVS 190
      | | | : || : ||| .           . . |
134  EIVPISNITENVYINLTCSSIHGYPEPKKMSVLLRTKNSTIEYDGIMQKS 183
      .           .           .           .
191  QDPETELYAVSSKLDF. ... NMTTNHSFMCLIKYGHLR. VNQTFNWNTTKQ 236
      || |||| || | . . | . | : : | . . |
184  QDNVTELYDVSISLSVSFPDVTSNMTIFCILETDKTRLLSSPFSIELEDP 233
      .           .           .           .
237  EHFPDNLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVR 286
      : || : | : : | : : . : | | .
234  QPPPDHIPWITAVLPTVVICVMVFCLILWKWKKKKRPRNSYKCGTNTMER 283
      .           .           .           .
287  PV..... 288
      .           .           .           .
284  EESEQTKKREKIHIPERSDEAQRVFKSSKTSSCDKSDTCF 323

```

FIG. 19.

mB7RP-2 Nucleotide sequence

ATGCTTCGAGGATGGGGTGGCCCCAGTGTGGGTGTGTGTGTGCGCACAGCGCTGGGGGT  
GCTGTGCCTCTGCCTCACAGGAGCTGTGGAAGTCCAGGTCTCTGAAGACCCCGTGGTGG  
CCCTGGTGGACACGGATGCCACCCTACGCTGCTCCTTTTCCCCAGAGCCTGGCTTCAGT  
CTGGCACAGCTCAACCTCATCTGGCAGCTGACAGACACCAAACAGCTGGTGCACAGCTT  
CACGGAGGGCCGGGACCAAGGCAGTGCCTACTCCAACCGCACAGCGCTCTTCCCTGACC  
TGTTGGTGCAAGGCAATGCGTCCTTGAGGCTGCAGCGCGTCCGAGTAACCGACGAGGGC  
AGCTACACCTGCTTTGTGAGCATTACAGGACTTTGACAGCGCTGCTGTTAGCCTGCAGGT  
GGCCGCCCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTACGTCCAG  
GGAACATGGTGACCATCACGTGCTCTAGCTACCAGGGCTATCCGGAGGCCGAGGTGTTT  
TGGAAGGATGGACAGGGAGTGCCCTTGACTGGCAATGTGACATCCCAGATGGCCAACGA  
GCGGGGCTTGTTTCGATGTTTACAGCGTCTGAGGGTGGTGCTGGGTGCTAACGGCACCT  
ACAGCTGCCTGGTACGCAACCCGGTGTGTCAGCAAGATGCTCACGGCTCAGTCACCATC  
ACAGGGCAGCCCCTGACATTCCCCCCTGAGGCTCTGTGGGTAACCGTGGGGCTCTCTGT  
CTGTCTTGTGGTACTACTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAGATCAAGCAGA  
GCTGCGAGGAGGAGAATGCAGGTGCCAAGGACCAGGATGGAGATGGAGAAGGATCCAAG  
ACAGCTCTACGGCCTCTGAAACCCTCTGAAAACAAAGAAGATGACGGACAAGAAATTGC  
TTGA

**FIG. 20.**

mB7RP-2 Protein sequence

MLRGWGGPSVGVCVRTALGVLCCLTGAVEVQVSEDPVVALVDTDATLRCSFSPEPGFS  
LAQLNLIWQLTDTKQLVHSFTEGRDQGSAYSNRALFPDLLVQGNASRLQRVRVTDEG  
SYTCFVSIQDFDSAASVSLQVAAPYSKPSMTLEPNKDLRPGNMVTITCSSYQGYPEAEVF  
WKDGGGVPLTGNVTSQMANERGLFDVHSLRVVVLGANGTYSCLVRNPVLQQDAHGSVTI  
TGQPLTFPPEALWTVGLSVCLVLLVALAFVCWRKIKQSCEEENAGAKDQDGDGEGSK  
TALRPLKPSENKEDDGQEIA.

**FIG. 21.**

Gap of: mB7RP-2 aa from: 1 to: 315 to: hB7RP-2 aa from: 1 to: 316  
Percent Similarity: 89.841 Percent Identity: 88.254

[illegible]

FIG. 22.

40/47

mB7RP-1 vs mB7RP-2

Gap of: mB7RP-1 aa from: 1 to: 322 to: mB7RP-2 aa from: 1 to: 315

Percent Similarity: 32.192 Percent Identity: 27.740

```

      .           .           .           .
1  MQLKPCFCVSLGTRQPVWKKLHVSSGFFSGLGLFLLLLSSLCAAS. AETE  49
      |   |   . ||.  ||.   . |
1  .....MLRGWGGPSVGVCVRTALGVLCCLTGAVEVQVSEDP  37
      .           .           .           .
50 VGAMVGSNNVLSCIDPHRRHFNLSGLYVYWQIENPEVSVTYYPYKSPGI  99
   | ||. .  | |   . |. | . ||. .  | : : |
38 VVALVDTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQG.  86
      .           .           .           .
100 NVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRVFMNTATELV 149
    |. | || | | : ||| || |. | | : || |
87 ...SAYSNRTALFPDLLVQGNASRLRQVRVTDEGSYTCFV.....SIQ 127
      .           .           .           .
150 KILEEVRLRVAANFSTPVIISTDSSN..PGQERTYTCMSKNGYPEPNLY 197
    | |. ||| . | | . .  || | || | ||| .
128 DFDSAASLQVAAPYSKPSMTLEPNKDLRPGNMVTITCSSYQGYPEAEVF 177
      .           .           .           .
198 WINTTDSLIDTALQNNTVYLNKLGlyDVISTLRLPWTSRGDVLCCVENV 247
    | | | :   .  |. ||: || | ||. .  | || |
178 W...KDGQGVPLTGNVTSQMANERGLFDVHSVLRVVLGANGTYSCLVRNP 224
      .           .           .           .
248 ALHQNITSISQAESFTGNNTKNPQETHNNELKVLVPVLAVLAAAFVSFI 297
    | |. . .  || | | . . |. . . | || |
225 VLQQDAHG...SVTITGQPLTFPEALWVTVGLSVCLVLLVALAFVCWR 271
      .           .           .           .
298 IYRRTRPHRSYTGPKTVQLELTDHA..... 322
    :. . . | | :
272 KIKQSCEEN. AGAKDQDGDGEGSKTALRPLKPSENKEDDGQEIA 315

```

**FIG. 23.**



41/47

mB7-H2 orf

ATGCTGCTCCTGCTGCCGATACTGAACCTGAGCTTACAACCTTCATCCTGTAGCAGCTTTATTCACCGTGACA  
GCCCCCTAAAGAAGTGTACACCGTAGACGTCGGCAGCAGTGTGAGCCTGGAGTGCGATTTTGACCGCAGAGAA  
TGCACTGAACTGGAAGGGATAAGAGCCAGTTTGCAGAAGGTAGAAAATGATACGTCTCTGCAAAGTGAAAGA  
GCCACCCTGCTGGAGGAGCAGCTGCCCCCTGGGAAAGGCTTTGTTCCACATCCCTAGTGTCCAAGTGAGAGAT  
TCCGGGCAGTACCGTTGCCTGGTCATCTGCGGGGCCGCTGGGACTACAAGTACCTGACGGTGAAAGTCAAA  
GCTTCTTACATGAGGATAGACACTAGGATCCTGGAGGTTCCAGGTACAGGGGAGGTGCAGCTTACCTGCCAG  
GCTAGAGGTTATCCCCTAGCAGAAGTGTCTGGCAAATGTCAGTGTTCTGCCAACACCAGCCACATCAGG  
ACCCCCGAAGGCCTCTACCAGGTCACCAAGTGTCTGCGCCTCAAGCCTCAGCCTAGCAGAACTTCAGCTGC  
ATGTTCTGGAATGCTCACATGAAGGAGCTGACTTCAGCCATCATTGACCCTCTGAGTCGGATGGAACCCAAA  
GTCCCCAGAACGTGGCCACTTCATGTTTTTCATCCCGCCTGCACCATCGCTTTGATCTTCTGGCCATAGTG  
ATAATCCAGAGAAAGAGGATCTAG

FIG. 24.

42/47

mB7-H2 Protein Sequence

Met	Ile	Phe	Leu	Leu	Leu	Met	Leu	Ser	Leu	Glu	Leu	Gln	Leu	His	Gln
1				5					10					15	
Ile	Ala	Ala	Leu	Phe	Thr	Val	Thr	Val	Pro	Lys	Glu	Leu	Tyr	Ile	Ile
			20					25					30		
Glu	His	Gly	Ser	Asn	Val	Thr	Leu	Glu	Cys	Asn	Phe	Asp	Thr	Gly	Ser
		35					40					45			
His	Val	Asn	Leu	Gly	Ala	Ile	Thr	Ala	Ser	Leu	Gln	Lys	Val	Glu	Asn
	50					55					60				
Asp	Thr	Ser	Pro	His	Arg	Glu	Arg	Ala	Thr	Leu	Leu	Glu	Glu	Gln	Leu
65					70					75					80
Pro	Leu	Gly	Lys	Ala	Ser	Phe	His	Ile	Pro	Gln	Val	Gln	Val	Arg	Asp
				85					90					95	
Glu	Gly	Gln	Tyr	Gln	Cys	Ile	Ile	Ile	Tyr	Gly	Val	Ala	Trp	Asp	Tyr
			100					105					110		
Lys	Tyr	Leu	Thr	Leu	Lys	Val	Lys	Ala	Ser	Tyr	Arg	Lys	Ile	Asn	Thr
		115					120					125			
His	Ile	Leu	Lys	Val	Pro	Glu	Thr	Asp	Glu	Val	Glu	Leu	Thr	Cys	Gln
	130					135					140				
Ala	Thr	Gly	Tyr	Pro	Leu	Ala	Glu	Val	Ser	Trp	Pro	Asn	Val	Ser	Val
145					150					155					160
Pro	Ala	Asn	Thr	Ser	His	Ser	Arg	Thr	Pro	Glu	Gly	Leu	Tyr	Gln	Val
				165					170					175	
Thr	Ser	Val	Leu	Arg	Leu	Lys	Pro	Pro	Pro	Gly	Arg	Asn	Phe	Ser	Cys
			180					185					190		
Val	Phe	Trp	Asn	Thr	His	Val	Arg	Glu	Leu	Thr	Leu	Ala	Ser	Ile	Asp
		195					200					205			
Leu	Gln	Ser	Gln	Met	Glu	Pro	Arg	Thr	His	Pro	Thr	Trp	Leu	Leu	His
	210					215					220				
Ile	Phe	Ile	Pro	Ser	Cys	Ile	Ile	Ala	Phe	Ile	Phe	Ile	Ala	Thr	Val
225					230					235					240
Ile	Ala	Leu	Arg	Lys	Gln	Leu	Cys	Gln	Lys	Leu	Tyr	Ser	Ser	Lys	Asp
				245					250					255	
Thr	Thr	Lys	Arg	Pro	Val	Thr	Thr	Thr	Lys	Arg	Glu	Val	Asn	Ser	Ala
			260					265					270		
Ile															

FIG. 25.

mB7-H2 orf vs hB7-H2 long orf

Gap of: hB7-H2 long from: 1 to: 822 to: mB7-H2 from: 1 to: 744

Percent Similarity: 78.331 Percent Identity: 78.331

```

      .       .       .       .
1  ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGAT  50
   ||| |  ||| ||| ||  ||  ||| |||  ||  || ||| ||| |  |
1  ATGCTGCTCCTGCTGCCGATACTGAACCTGAGCTTACAACCTTCATCCTGT  50

      .       .       .       .
51 AGCAGCTTTATTACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGC 100
   ||||| ||||| ||||| ||||| ||| |||||  |||
51 AGCAGCTTTATTACCGTGACAGCCCCTAAAGAAGTGTACACCGTAGACG 100

      .       .       .       .
101 ATGGCAGCAATGTGACCCTGGAATGCAACTTTGA. CACTGGAAGTCATGT 149
     ||||| |||| ||||| ||| | |||| | | | | | |
101 TCGGCAGCAGTGTGAGCCTGGAGTGCGATTTTGACCGCAGAGAATGCACT 150

      .       .       .       .
150 GAACCTTGGAGCAATAACAGCCAGTTTGCAAAAGGTGGAAAATGATACAT 199
     ||| || | || |||| ||||| ||||| |||| ||||| |||
151 GAA. CTGGAAGGGATAAGAGCCAGTTTGCAAGGTAGAAAATGATACGT 199

      .       .       .       .
200 CCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCTAGGG 249
   | |  ||  ||||| ||||| ||||| ||||| ||||| |||
200 CTCTGCAAAGTGAAAGAGCCACCCTGCTGGAGGAGCAGCTGCCCTGGGA 249

      .       .       .       .
250 AAGGCCTCGTTCCACATACCTCAAGTCCAAGTGAGGGACGAAGGACAGTA 299
     |||| | ||||| ||| ||| ||||| ||  || |||||
250 AAGGCTTTGTTCCACATCCCTAGTGTCCAAGTGAGAGATTCCGGGCAGTA 299

      .       .       .       .
300 CCAATGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTC 349
     ||  ||| |  ||||| |||| ||||| ||||| ||||| |||
300 CCGTTGCCTGGTCATCTGCGGGCCGCCTGGGACTACAAGTACCTGACGG 349

      .       .       .       .
350 TGAAAGTCAAAGCTTCCTACAGGAAAATAAACACTCACATCCTAAAGGTT 399
     ||||| ||||| |||| ||  ||| |||||  |||| |||||
350 TGAAAGTCAAAGCTTCTTACATGAGGATAGACACTAGGATCCTGGAGGTT 399

```

**FIG. 26A.**

400 CCAGAAACAGATGAGGTAGAGCTACCTGCCAGGCTACAGGTTATCCTCT 449  
|||| ||| |||| ||| ||||||||| ||||||| ||  
400 CCAGGTACAGGGGAGGTGCAGCTTACCTGCCAGGCTAGAGGTTATCCCCT 449  
450 GGCAGAAGTATCCTGGCCAAACGTCAGCGTTCCTGCCAACACCAGCCACT 499  
||||||| ||||||| || ||||| ||||||||| ||||||| ||  
450 AGCAGAAGTGTCTGGCAAAATGTCAGTGTTCCTGCCAACACCAGCCACA 499  
500 CCAGGACCCCTGAAGGCCTCTACCAGGTCACCAGTGTTCGCGCCTAAAG 549  
||||||| ||||||||| ||||||||| ||||||||| ||||| |||  
500 TCAGGACCCCGAAGGCCTCTACCAGGTCACCAGTGTTCGCGCCTCAAG 549  
550 CCACCCCTGGCAGAACTTCAGCTGTGTTCCTGGAATACTCACGTGAG 599  
|| | ||| ||||||||| ||||| ||||| ||||| |||  
550 CCTCAGCCTAGCAGAACTTCAGCTGCATGTTCTGGAATGCTCACATGAA 599  
600 GGAACCTACTTTGGCCAGCATTGACCTTCAAAGTCAGATGGAACCCAGGA 649  
||| || |||| |||| ||||||| || |||| |||||||||  
600 GGAGCTGACTTCAGCCATCATTGACCTCTGAGTCGGATGGAACCCAAAG 649  
650 CCCATCCAACCTGGCTGCTTCACATTTTCATCCCCTCCTGCATCATTGCT 699  
|| ||| |||| |||| ||||||| ||||| ||| |||  
650 TCCCAGAACGTGGCCACTTCATGTTTCATCCCGGCCTGCACCATCGCT 699  
700 TTCATTTTCATAGCCACAGTGATAGCCCTAAGAAAACAACCTCTGTCAAAA 749  
|| || ||| || |||| |||||| || |||| |||  
700 TTGATCTTCCTGGCCATAGTGATAATCCAGAGAAAGAGGATCTAG..... 744

FIG. 26B.

mB7-H2 vs hB7-H2 long

Gap of: mB7-H2 aa from: 1 to: 247 to: hB7-H2 long aa from: 1 to: 273

Percent Similarity: 74.899 Percent Identity: 69.636

```
1 MLLLLPILNLSLQLHPVAALFTVTAPKEVYTVDVGSSVSLECDRRECT 50
  | | . | . | | | | : | | | | | | | | | | : | | . | | | . | |
1 MIFLLMLSLQLHQIAALFTVTPKELYIEHGSNVTLECNFDTGSHV 50

51 ELEGIRASLQKVENDTSLQSERATLLEEQLPLGKALFHIPSVQVRDSGQY 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 NLGAITASLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQY 100

101 RCLVICGAADYKYLTVKVKASYMRIDTRILEVPGTGEVQLTCQARGYPL 150
  . | : | | | | | | | | | | | | | | | | | | | | | | | | | |
101 QCIIYGVADYKYLTLKVKASYRKINTHILKVPETDEVELTCQATGYPL 150

151 AEVSWQNVSPANTSHIRTPEGLYQVTSVLRLKPQPSRNFSCMFVNAHMK 200
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 AEVSWPNVSPANTSHSRTPEGLYQVTSVLRLKPPPGRNFSCVFWNTHVR 200

201 ELTSAIIDPLSRMEPKVPRTWPLHVFIPACTIALIFLAIVIIQRKRI... 247
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 ELTLASIDLQSQMEPRTHPTWLLHIFIPSCIIAFIFATVIALRKQLCQK 250
```

⋮

FIG. 27.

mB7-H2 vs mB7-H1

Gap of: mB7-H2 aa from: 1 to: 247 to: mB7-H1 aa from: 1 to: 290  
Percent Similarity: 44.262 Percent Identity: 34.016

```
1 . MRIFAGIIFTACCHLLRA. FTITAPKDLVVEYGSNVTMECRFPVEREL 48
: : : . | . | ||:||||:| |: ||.|.:|| |
1 MLLLLPILNLSLQLHPVAALFTVTAPKEVYTVDVGSSVSLECDRRECT 50
49 DLLALVYWEKEDEQVIQFVAGEEDLKQHSNFRGRASLPKDQLLKGNAA 98
:| : :| | : |. : ||. |.:|| | |
51 ELEGI.....RASLQKVENDTSLQSE.....RATLLEEQLPLGKAL 86
99 LQITDVKLQDAGVYCCIISYGA. DYKRITLKVNPYRKINQRISVDPAT 147
| |...|. | | | : | | | | | | : |. | | |
87 FHIPSVQVRDSGQYRCLVICGAAWDYKYLTVKVKASYMRIDTRILEVPGT 136
148 SEHELICQAEGYPEAEVIWTNSDHQPVSGKRSVTTSRTEGMLLNVTSSLR 197
| :| ||| ||| ||| | | || . . || | ||| ||
137 GEVQLTCQARGYPLAEVSWQN....VSPANTSHIRTPEGLYQVTSVLR 181
198 VNATANDVFYCTFWRSQPGQNHTAELIPELPATHPPQNRTHWVLLGSIL 247
. . | | | . : . | : |. | : .
182 LKPQPSRNFSCMFVNAHMKELTS A I I D P L S R M E P K V P R T W P L H V F I P A C T 231
248 LFLIVVSTVLLFLRKQVRMLDVEKCGVEDTSSKNRNDTQFEET 290
: || . . | : | : | :
232 IALIFLAIVII. QRKRI.....247
```

FIG. 28.

mB7-H2 vs mB7RP-2

Gap of: mB7-H2 aa from: 1 to: 247 to: mB7RP-2 aa from: 1 to: 298

Percent Similarity: 32.245 Percent Identity: 24.490

```
1 MLRGWGGPSVGVCVRTALGVLCLCLTGAVEVQVSEDPVVALVDTDATLRC 50
      | | . . . | | | |
1 ..... MLLLLPILNLSLQLHPVAALFTVTAPKEV 29
51 . SFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYSNRTALFPDL 99
      | | : | : : | . . | | | | :
30 YTVDVGSSVSLECDFDRRECTELEGIRASLQKVENDTSLQSERATLLEEQ 79
100 LVQGNASRLQRVRVTDEGSYTCFVSI. QDFDSAASLQVAAPYSKPSMT 148
      | | | : | | | | | . | . . . | | | :
80 LPLGKALFHIPSVQVRDSGQYRCLVICGAADYKYLTVKVKASYMRIDTR 129
149 LEPNKDLRPGNMVTITCSSYQGYPEAEVFWKDGGGVPLTGNVTSQMANER 198
      : : | : | | . | | | | | | | | | |
130 I... LEVPGTGEVQLTCQA. RGYPLAEVSW... QNVSVPAN. TSHIRTP 171
199 GLFDVHSVLRVVLGANGTYSLVRNPVLQQDAHGSVTITGQPLTFPPEAL 248
      ||: | ||| . : ||: | : : : : |
172 GLYQVTSVLRLKPQPSRNFSCMFNAHMKELTSAAIIDPLSRMEPKVPRTW 221
249 WVTVGLSVCLVLLVALAFVCRKIKQSCÉEENAGAKDQDGDGEGSKTAL 298
      . | : | : | : | |
222 PLHVFIPACTIALIFLAIVIIQRKRI..... 247
```

⋮

FIG. 29.